Amendments to the Claims

Please amend claims 1 and 13-16 as indicated below in the listing of claims.

Listing of Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently amended) A method of identifying a WW domain binding agent, said method comprising:

(a) defining an interaction site of a WW domain based on a plurality of atomic coordinates of said WW domain **obtained from a WW domain crystallized in co-complex with a known WW domain binding agent, substrate, or inhibitor**;

(b) modeling a potential binding agent that fits spatially into said interaction site;

(c) contacting said potential binding agent with said WW domain in the presence of a WW domain substrate; and

(d) determining the ability of said potential binding agent to compete with said WW domain substrate for binding to said WW domain.

2. (Original) The method of claim 1, wherein said WW domain is a PIN1 WW domain.

3. (Original) The method of claim 1, wherein said binding agent is an agonist or antagonist of said WW domain.

4. (Original) The method of claim 1, wherein said binding agent is an inhibitory agent.

5. (Original) The method of claim 4, wherein the inhibitory agent is designed from a known inhibitor.

6. (Original) The method of claim 1, wherein said binding agent is a peptide.

7. (Original) The method of claim 6, wherein said binding agent has a sequence Tyr-pSer-Pro-Thr-pSer-Pro-Ser (SEQ ID NO:3).

8. (Original) The method of claim 1, wherein said binding agent is selected from the group consisting of a small molecule, a peptidomimetic, and an antibody.

9. (Original) The method of claim 1, wherein said binding agent is selected by providing a computer with a three-dimensional representation of said interaction site and using a computer algorithm to predict a three-dimensional representation of said potential binding agent.

10. (Original) The method of claim 1, wherein said plurality of atomic coordinates are as set forth in Table 1.

11. (Original) The method of claim 1, wherein said potential binding agent is designed de novo.

12. (Original) A WW domain binding agent identified by the method of claim 1.

13. (Currently amended) A method of identifying a WW domain binding agent, said method comprising:

defining an interaction site of a WW domain based on a plurality of atomic coordinates of said WW domain **obtained from a WW domain crystallized in co-complex with a known WW domain binding agent, substrate, or inhibitor**;

modeling a potential binding agent that fits spatially into said interaction site;

determining the ability of said potential binding agent to compete with a WW domain substrate for said interaction site by contacting said potential binding agent with said WW domain in the presence of said WW domain substrate.

14. (Currently amended) A method of identifying a WW domain binding agent, said method comprising:

modeling a potential binding agent that fits spatially into an interaction site of a WW domain defined by a plurality of atomic coordinates of said WW domain **obtained from a WW domain crystallized in co-complex with a known WW domain binding agent, substrate, or inhibitor**;

contacting said potential binding agent with said WW domain in the presence of a WW domain substrate; and

determining the ability of said potential binding agent to compete with said WW domain substrate for binding to said WW domain.

15. (Currently amended) A method of identifying a WW domain binding agent, said method comprising:

(a) modeling a potential binding agent that fits spatially into an interaction site of a WW domain defined by a plurality of atomic coordinates of said WW domain **obtained from a WW domain crystallized in co-complex with a known WW domain binding agent, substrate, or inhibitor**; and

(b) determining the ability of said potential binding agent to compete with a WW domain substrate for said interaction site by contacting said potential binding agent with said WW domain in the presence of said WW domain substrate.

16. (Currently amended) A method of identifying a WW domain binding agent, said method comprising:

determining the ability of a potential binding agent to compete with a WW domain substrate for binding to a WW domain, wherein the potential binding agent is modeled to fit spatially into a WW domain interaction site defined by a plurality of atomic coordinates **obtained from a WW domain crystallized in co-complex with a known WW domain binding agent, substrate, or inhibitor**.

17. (Withdrawn) A computer program on a computer readable medium, said computer program comprising instructions to cause a computer to:

define an interaction site of a WW domain based on a plurality of atomic coordinates of said WW domain; and

model a potential binding agent that fits spatially into said interaction site.

18. (Withdrawn) A computer program on a computer readable medium, said computer program comprising instructions to cause a computer to:

model a potential binding agent that fits spatially into a WW domain interaction site defined by a plurality of atomic coordinates.

19. (Withdrawn) An isolated crystalline WW domain.

20. (Withdrawn) The crystalline WW domain of claim 19, wherein said WW domain is a Pin1 WW domain.

21. (Withdrawn) The crystalline WW domain of claim 20, wherein said Pin1 WW domain has a sequence as set forth in SEQ ID NO:2.

22. (Withdrawn) The crystalline WW domain of claim 20, wherein said atomic coordinates of the atoms of said WW domain are as set forth in Table 1.

23. (Withdrawn) A crystalline complex comprising an isolated WW domain and a WW domain binding agent.

24. (Withdrawn) The crystalline complex of claim 23, wherein said WW domain is a Pin1 WW domain.

25. (Withdrawn) The crystalline complex of claim 24, wherein said Pin1 WW domain has a sequence as set forth in SEQ ID NO:2.

26. (Withdrawn) The crystalline complex of claim 23, wherein said atomic coordinates of the atoms of said WW domain are as set forth in Table 1.

27. (Withdrawn) The crystalline complex of claim 23, wherein said binding agent is a C-terminal domain of RNA polymerase II.

28. (Withdrawn) The cyrstalline complex of claim 23, wherein said binding agent has a sequence Tyr-pSer-Pro-Thr-pSer-Pro-Ser (SEQ ID NO:3).